AMENDMENTS TO THE CLAIMS

This listing of claims replaces all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Original) A cell comprising at least:

- a first conjugate comprising a first protein and the N-terminal fragment of complementation protein; and
- a second conjugate comprising a second protein and the C-terminal fragment of the complementation protein;

wherein said first conjugate has a predominant location in a different cellular location from where said second conjugate is predominantly located,

wherein said first protein and said second protein will bind to each other, and

wherein said complementation protein exhibits altered characteristics when the two fragments of the complementation protein are brought into close apposition and the two fragments of the complementation protein form the full functional protein.

2. (Currently Amended) The cell according to ~~any~~ claim 1, wherein the cellular compartment of the first conjugate is determined by the nature of the first protein.

3. (Previously Presented) The cell according to claim 1, wherein the cellular compartment of the second conjugate is determined by the nature of the second protein.

4. (Previously Presented) The cell according to claim 1, wherein the second conjugate further comprises an anchor protein, wherein said anchor protein is anchored in a different cellular compartment from where said first protein is predominantly located.

5. (Original) A cell comprising at least:

- a first conjugate comprising a first protein, interaction partner A and the first terminal fragment of a complementation protein; and

- a second conjugate comprising a interaction partner B and the second terminal fragment of the complementation protein;

wherein said first conjugate has a predominant location in a different cellular compartment from where said second conjugate is predominantly located,

wherein said complementation protein exhibits altered characteristics when the two fragments of the complementation protein are brought into close apposition and the two fragments of the complementation protein form the full functional protein.

6. (Original) The cell according to claim 5, wherein said interaction partner A and interaction partner B bind to each other.

7. (Original) The cell according to claim 5, wherein said interaction partner A and interaction partner B bind to each other only when an interaction stimulus has been applied.

8. (Previously Presented) The cell according to claim 5, wherein the second conjugate further comprises an anchor protein, wherein said anchor protein is anchored in a different cellular compartment from where said first protein is predominantly located.

9. (Withdrawn) The cell according to claim 5, wherein complementation protein is dihydrofolate reductase (DHFR).

10. (Withdrawn) The cell according to claim 1, wherein the complementation protein is Ubiquitin.

11. (Withdrawn) The cell according to claim 1, wherein complementation protein is β-lactamase.

12. (Withdrawn) The cell according to claim 1, wherein complementation protein is β-galactosidase.

13. (Withdrawn) The cell according to claim 1, wherein complementation protein is a fluorescent protein.

14. (Original) The cell according to claim 13, wherein the complementation protein is Green Fluorescent Protein (GFP).

15. (Original) The cell according to claim 14, wherein the complementation protein is derived from *Aequoria Victoria.*

16. (Original) The cell according to claim 14, wherein N-terminal fragment of the complementation protein is an N-terminal fragment of GFP, comprising a continuous stretch of amino acids from amino acid number 1 to amino acid number X of GFP, wherein the peptide bond between amino acid number X and amino acid number X+1 is within a loop of GFP and C-terminal fragment of the complementation protein is a C-terminal fragment of GFP, comprising a continuous stretch of amino acids from amino acid number X+1 to amino acid number 238 of GFP.

17. (Original) The cell according to claim 14, wherein the N-terminal fragment of the complementation protein is an N-terminal fragment of GFP, comprising a continuous stretch of amino acids from amino acid number 1 to amino acid number X of GFP, wherein the peptide bond between amino acid number X and amino acid number X+1 is within a loop of GFP and the C-terminal of the complementation protein is a C-terminal fragment of GFP, comprising a continuous stretch of amino acids from amino acid number Y+1 to amino acid number 238 of GFP, wherein Y<X creating an overlap of the two GFP fragments, and wherein the peptide bond between amino acid Y and amino acid Y+1 is within a loop of GFP.

18. (Previously Presented) The cell according to claim 14, wherein GFP is selected from the group consisting of EGFP, EYFP, ECFP, dsRed and Renilla GFP.

19. (Original) The cell according to claim 18, wherein the GFP is EGFP.

20. (Original) The cell according to claim 18, wherein the GFP is EYFP.

21. (Previously Presented) The cell according to claim 14, wherein the amino acid in position 1 preceding the chromophore has been mutated to provide an increase of fluorescence intensity.

22. (Original) The cell according to claim 21, wherein the amino acid F in position 1 preceding the chromophore has been substituted by L.

23. (Previously Presented) The cell according to claim 14, wherein the GFP has been mutated to further contain the S72A mutation.

24. (Previously Presented) The cell according to claim 16, wherein X is between 9 and 10 within the Thr9-Val11 loop; or between 23 and 24 within the Asn23-His25 loop; or between 38 and 39 within the Thr38-Gly40 loop; or between 48 and 55 within the Cys48-Pro56 loop; or between 72 and 75 within the Ser72-Asp76 loop; or between 81 and 82 within the His81-Phe83 loop; or between 88 and 89 within the Met88-Glu90 loop; between 101 and 102 within the Lys101-Asp103 loop; or between 114 and 117 within the Phe114-Thr118 loop; or between 128 and 144 within the Ile 128-Tyr145 loop; or between 154 and 159 within the Ala154-Gly160 loop; or between 171 and 174 within the Ile171-Ser175 loop; or between 188 and 196 within the Ile188-Asp197 loop; or between 210 and 214 within the Asp210-Art215 loop.

25. (Original) The cell according to claim 24, wherein X is between 154 and 159 within the Ala154-Gly160 loop.

26. (Original) The cell according to claim 25, wherein X is 157 within the Ala154-Gly160 loop.

27. (Original) The cell according to claim 24, wherein X is between 171 and 174 within the Ile171-Ser175 loop.

28. (Original) The cell according to claim 27, wherein X is 172 within in Ile171-Ser175 loop.

29. (Original) The cell according to claim 17, wherein Y is between 154 and 159 within the Ala154-Gly160 loop.

30. (Original) The cell according to claim 29, wherein Y is 157 within the Ala154-Gly160 loop.

31. (Previously Presented) The cell according to claim 16, wherein X is 172 within in Ile171-Ser175 loop and wherein Y is 157 within the Ala154-Gly160 loop.

32. (Previously Presented) The cell according to claim 1, wherein the N-terminal fragment of the complementation protein is fused in frame with a first protein of interest.

33. (Previously Presented) The cell according to claim 1, wherein the first protein is fused to the N-terminal of the N-terminal fragment of the complementation protein.

34. (Previously Presented) The cell according to claim 1, wherein the first protein is fused to the C-terminal of the N-terminal fragment of the complementation protein.

35. (Previously Presented) The cell according to claim 1, wherein the C-terminal fragment of the complementation protein is fused in frame with the second protein.

36. (Previously Presented) The cell according to claim 1, wherein the second protein of interest is fused to the N-terminal of the C-terminal fragment of the complementation protein.

37. (Previously Presented) The cell according to claim 1, wherein the second protein of interest is fused to the C-terminal of the C-terminal fragment of the complementation protein.

38. (Previously Presented) The cell according to claim 1, wherein the N-terminal fragment of the complementation protein fused in frame to a first protein further comprises a linker sequence between the N-terminal fragment of the complementation protein and the first protein.

39. (Previously Presented) The cell according to claim 1, wherein the C-terminal fragment of the complementation protein fused in frame to a second protein further comprises a linker sequence between the C-terminal fragment of the complementation protein and the second protein.

40. (Previously Presented) The cell according to claim 14, wherein the GFP is EYFP further containing an F64L mutation, wherein X is 172, wherein the first protein fused to the N-terminal fragment of GFP is fused to the C-terminal of the N-terminal fragment of GFP and wherein the second protein fused to the C-terminal fragment of GFP is fused to the N-terminal of the C-terminal fragment of GFP.

41. (Previously Presented) The cell according to claim 14, wherein the GFP is EYFP further containing an F64L mutation, wherein X is 157, wherein the first protein fused to the N-terminal fragment of GFP is fused to the C-terminal of the N-terminal fragment of GFP and wherein the second protein fused to the C-terminal fragment of GFP is fused to the N-terminal of the C-terminal fragment of GFP.

42. (Previously Presented) The cell according to claim 1, wherein the first conjugate is expressed in the cell.

43. (Previously Presented) The cell according to claim 1, wherein the second conjugate is expressed in the cell.

44. (Withdrawn - Currently Amended) The cell according to claim 5, wherein interaction partner A is FKBP12, interaction partner B is FRAP (or vise versa) and ~~the~~ an interaction stimulus is Rapamycin.

45. (Currently Amended) The cell according to claim 5, wherein interaction partner A is FKBP12, interaction partner B is FRB (T2098L) (or vise versa) and ~~the~~ an interaction stimulus is Rapamycin.

46. (Withdrawn - Currently Amended) The cell according to claim 5, wherein interaction partner A is FKBP12, interaction partner B is FRB (T2098L) (or vise versa) and ~~the~~ an interaction stimulus is AP21967.

47. (Withdrawn - Currently Amended) The cell according to claim 5, wherein interaction partner A is FKBP12, interaction partner B is FKBP12 (or vise versa) and ~~the~~ an interaction stimulus is AP21967.

48. (Withdrawn - Currently Amended) The cell according to claim 5, wherein interaction partner A is FKBP12, interaction partner B is FKBP12 (or vise versa) and ~~the~~ an interaction stimulus is AP21967.

49. (Withdrawn - Currently Amended) The cell according to claim 5, wherein interaction partner A and B are steroid hormone receptors and ~~the~~ a dimerizing agent is the cognate hormone ligand.

50. (Withdrawn - Currently Amended) The cell according to claim 5, wherein interaction partner A and B are estrogen receptors and ~~the~~ an interaction stimulus agent is estrogen.

51. (Withdrawn) The cell according to claim 4, wherein the anchor protein is a protein containing the transmembrane domain of the epidermal growth factor receptor (EGFR), or containing the transmembrane domain of one of the integrin protein family, or containing the myristoylation sequence from c-Src (residues 1-14).

52. (Withdrawn) The cell according to claim 4, wherein the anchor protein is a histone protein or a protein normally restricted to nucleoli, for example the p120 nucleolar protein.

53. (Withdrawn) The cell according to claim 4, wherein the anchor protein is a protein normally confined to mitochondrial outer or inner membranes for example VDAC, F_0 subunit of ATP-ase, or NADH dehydrogenase.

54. (Withdrawn) The cell according to claim 4, wherein the anchor protein is a protein normally confined to the various different regions of Golgi bodies for example TGN38 or ADAM12-L.

55. (Withdrawn) The cell according to claim 4, wherein the anchor protein is a protein normally confined to focal adhesion complexes for example P125, FAK, integerin alpha or beta, or paxillin.

56. (Withdrawn) The cell according to claim 4, wherein the anchor protein is a protein normally associated with cytoskeletal structures such as F-actin strands or micro tubular bundles for example MAP4, actin binding domain of alpha-actinin, kinesins, myosins or dyniens.

57. (Previously Presented) The cell according to claim 4, wherein the anchor protein is a protein normally associated with nuclear material or nuclear components, such as histone proteins, including histones H1, H2A, H2B, H3, H4, and variants thereof.

58. (Withdrawn) The cell according to claim 4, wherein the anchor protein is a protein

normally associated with nuclear membrane such as A and B type lamins, or associated with nuclear bodies such as splicing bodies, Cajal bodies, PML nuclear bodies (PML oncogenic domains, PODS), or transcription engines such as RNA polymerase POL-II.

59. (Previously Presented) A cell according to claim 1, where in the cell is an eukaryotic cell.

60. (Original) A cell according to claim 1, where in the cell is a prokaryotic cell.

61. (Withdrawn) A method for detecting protein-protein interactions comprising the steps of:

(a) providing a cell comprising at least:

- a first conjugate comprising the first protein of interest and the first terminal fragment of a complementation protein; and

- a second conjugate comprising the second protein of interest and the second terminal fragment of a complementation protein;

wherein said second protein of interest has a predominant location in a different cellular location from where said first protein of interest is predominantly located,

(b) determine if complementation partner A and complementation partner B has complemented;

complementation between complementation partner A and complementation partner B being indicative that the first protein of interest has translocated from the predominant location of this first protein of interest to the cellular compartment where the second protein of interest is located and that the two proteins of interest interact.

62. (Withdrawn) A method for detecting protein-protein interactions comprising the steps of:

(a) providing a cell according to claim 1, and

(b) determine if complementation partner A and complementation partner B has complemented;

complementation between complementation partner A and complementation partner B being indicative that the first protein of interest has translocated from the predominant location of this first protein of interest to the cellular compartment where the second protein of interest is located and that the two proteins of interest interact.

63. (Withdrawn) A method for testing if a compound prevents a protein-protein interaction comprising the steps of:

(a) providing a cell according to claim 1;

(a1) adding the compound to the cells of step (a);

(a2) adding a translocation stimulus to the cells of step (a1),

wherein the translocation stimulus causes the two conjugates to have the same cellular localization;

(b) determine if complementation partner A and complementation partner B has complemented;

less complementation compared to a system omitting step (a1) being indicate that the compound is capable of preventing the interaction between the two proteins.

64. (Withdrawn) A method according to claim 61, wherein the second conjugate further comprises an anchor protein, wherein said anchor protein is anchored in a different cellular compartment from where said first protein of interest is predominantly located.

65. (Withdrawn) A method for detecting translocation of a protein comprising the steps of: (a) providing a cell comprising at least:

- a first conjugate comprising said protein, the first terminal of the complementation protein, and interaction partner A; and

- a second conjugate comprising an anchor protein, the second terminal of complementation protein, and interaction partner B;

wherein said anchor protein is anchored in a different cellular compartment from where said protein is predominantly located;

and wherein said interaction partner A and interaction partner B bind to each other;

(b) determine if complementation partner A and complementation partner B has complemented;

complementation between complementation partner A and complementation partner B being indicative that said protein has translocated from the predominant location of the protein to the cellular compartment where the anchor protein is anchored.

66. (Withdrawn) A method for detecting translocation of a protein comprising the steps of:

(a) providing a cell according to claim 6, and

(b) determine if complementation partner A and complementation partner B has complemented;

complementation between complementation partner A and complementation partner B being indicative that said protein has translocated from the predominant location of the protein to the cellular compartment where the anchor protein is anchored.

67. (Withdrawn) A method for testing if a compound induces translocation of a protein comprising the steps of:

(a) providing a cell according to claim 6;

(a1) adding the compound to the cells of step (a);

(b) determine if complementation partner A and complementation partner B has complemented;

ncreased complementation compared to a system omitting step (a1) being indicate that the compound induces translocation of the protein.

68. (Withdrawn) A method for testing if a compound prevents translocation of a protein comprising the steps of:

(a) providing a cell according to claim 6;

(a1) adding the compound to the cells of step (a);

(a2) adding a translocation stimulus to the cells of step (a1):

(b) determine if complementation partner A and complementation partner B has complemented;

less complementation compared to a system omitting step (a1) being indicative that the compounds prevents translocation of the protein.

69. (Withdrawn) A method for detecting translocation of a protein comprising the steps of: (a) providing a cell comprising at least:

- a first conjugate comprising said protein, complementation partner A, and interaction partner A; and

- a second conjugate comprising an anchor protein, complementation partner B, and interaction partner B;

wherein said anchor protein is anchored in a different cellular compartment from where said protein is predominantly located,

wherein said interaction partner A and interaction partner B bind to each other only when an interaction stimulus has been applied;

(b) add an interaction stimulus;

(c) determine if complementation partner A and complementation partner B has complemented;

complementation between complementation partner A and complementation partner B being indicative that said protein has translocated from the predominant location of the protein to the cellular compartment where the anchor protein is anchored after addition of the interaction stimulus.

70. (Withdrawn) A method for detecting translocation of a protein comprising the steps of:

(a) providing a cell according to claim 7, and

(b) add an interaction stimulus;

(c) determine if complementation partner A and complementation partner B has complemented;

complementation between complementation partner A and complementation partner B being indicative that said protein has translocated from the predominant location of the protein to the cellular compartment where the anchor protein is anchored after addition of the interaction stimulus.

71. (Withdrawn) A method for testing if a compound induces translocation of a protein comprising the steps of:

(a) providing a cell according to claim 7;

(a1) adding the compound to the cells of step (a);

(b) add an interaction stimulus;

(c) determine if complementation partner A and complementation partner B has complemented;

increased complementation compared to a system omitting step (a1) being indicate that the compound induces translocation of the protein.

72. (Withdrawn) A method for testing if a compound prevents translocation of a protein comprising the steps of:

(a) providing a cell according to claim 7;

(a1) adding the compound to the cells of step (a);

(a2) adding a translocation stimulus to the cells of step (a1):

(b) add an interaction stimulus;

(c) determine if complementation partner A and complementation partner B has complemented;

less complementation compared to a system omitting step (a1) being indicative that the compound prevents translocation of the protein.

73. (Withdrawn) A kit for detecting antigens comprising:

(a) a first antibody that binds to the antigen;

(b) a first conjugate comprising a protein binding to the first antibody and the N-terminal of a complementation protein;

(c) a second conjugate comprising a protein binding to the first antibody and the C-terminal of the complementation protein;

whereby binding of the first and second conjugate to the first antibody will bring the two terminals of the complementation protein so close that a functional protein is formed.

74. (Withdrawn) A method for determining caspase activity in a cell comprising at least the steps of

(a) providing a cell comprising at least:

- a first conjugate comprising the first terminal of a complementation protein, interaction partner A, a nuclear localisation sequence (NLS), a Valine-Alanine-Aspartate (VAD) sequence and an anchor protein;

- a second conjugate comprising the second terminal of a complementation protein, interaction partner B and an anchor protein;

wherein the anchor protein of the first conjugate is in a different cellular location from the nucleus, and the anchor protein of the second conjugate is in the nucleus and

wherein interaction partner A, the NLS and the first terminal of the complementation protein are all located on the same side of the VAD sequence and the anchor protein is located on the other side of the NLS;

(b) determine if the complementation protein has complemented

complementation being indicative that caspase has cleaved the first conjugate and the free part has translocated to the nucleus and partner A and complementation partner B has complemented.

75. (Withdrawn) A nucleic acid encoding any of the conjugates, fragments or fusions proteins.